

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 6, 2004, 19:24:00 ; Search time 80.25 Seconds
(without alignments)
43.019 Million cell updates/sec

Title: US-10-618-644-3
Perfect score: 38
Sequence: 1 NWGPLV 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	257	Q6MP42	Q6mp42 bdellovibri
2	38	100.0	257	CAE78956	CAE78956 bdellovib
3	38	100.0	562	GLC4_SOYBN	P02858 glycine max
4	38	100.0	562	Q43452	Q43452 glycine soj
5	38	100.0	563	Q39921	Q39921 glycine soj
6	38	100.0	563	Q9SB11	Q9sb11 glycine max
7	37	97.4	483	Q6CLB6	Q6clb6 kluyveromyc
8	37	97.4	683	Q892S9	Q892s9 bacteroides
9	36	94.7	724	Q788R9	Q788r9 neurospora
10	36	94.7	793	Q6F9M7	Q6f9m7 acinetobact
11	35	92.1	204	CEA_ECOLI	Q47108 escherichia
12	35	92.1	378	Q72A77	Q72a77 penicillium
13	35	92.1	387	CEAN_ECOLI	P08083 escherichia
14	35	92.1	499	Q9XB77	Q9xb77 escherichia
15	35	92.1	510	CEAB_ECOLI	P05819 escherichia
16	35	92.1	592	CEA_CITFR	P04480 citrobacter
17	35	92.1	611	Q8SBG9	Q8sbg9 bacterioph
18	35	92.1	619	Q24681	Q24681 shigella bo
19	35	92.1	629	Q9KJ98	Q9kj98 escherichia
20	35	92.1	657	Q8NUN0	Q8njo0 aspergillus
21	35	92.1	666	Q7SDR8	Q7sdr8 neurospora
22	35	92.1	858	Q7Q6R9	Q7q6r9 anopheles g
23	35	92.1	1073	Q3GUN3	Q3gun3 caenorhabdi
24	34	89.5	178	Q6NDI7	Q6ndi7 rhodopsedu
25	34	89.5	178	CAE25565	CAE25565 rhodopseu
26	34	89.5	250	Q7DM64	Q7dm64 arabisdopeis
27	34	89.5	261	Q6HMR9	Q6hmr9 bacillus th
28	34	89.5	265	Q9K7I7	Q9k7i7 bacillus ha
29	34	89.5	325	Q9AM28	Q9am28 xanthomonas
30	34	89.5	336	Q9PET8	Q9pet8 xanthomonas
31	34	89.5	340	O04348	O04348 arabidopsis

32	34	89.5	344	1	HIFN_BRARE	P59723 brachydanio
33	34	89.5	367	2	Q8LEC9	Q8lec9 arabidopsis
34	34	89.5	367	2	Q9M9Z2	Q9m9z2 arabidopsis
35	34	89.5	431	2	Q8ZT65	Q8zt65 pyrobaculum
36	34	89.5	449	2	Q7PT63	Q7pt63 anopheles g
37	34	89.5	464	2	Q6EQK9	Q6eqk9 oryza sativ
38	34	89.5	470	2	Q0S351	Q0s351 entamoeba h
39	34	89.5	470	2	Q0Y0D0	Q0y0d0 oryza sativ
40	34	89.5	499	2	Q7UY60	Q7uy60 rhodopirell
41	34	89.5	539	2	Q9USK3	Q9usk3 schizosacch
42	34	89.5	586	2	Q67335	Q67335 aquifex aeo
43	34	89.5	593	2	Q66826	Q66826 aquifex aeo
44	34	89.5	616	2	Q7KR41	Q7kr41 drosophila
45	34	89.5	616	2	AA68656	AA68656 drosophila

ALIGNMENTS

RESULT 1
Q6MP42 PRELIMINARY; PRT; 257 AA.
AC Q6MP42; PRELIMINARY; PRT; 257 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE ABC-type transport system permease protein.
GN Name=glpF; OrderedLocusNames=Bdi024;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP -SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Kellner H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
genomic perspective".
RL Science 303:689-692(2004).
DR EMBL; BX842648; CAE78956.1; -.
KW Complete proteome.
SQ SEQUENCE 257 AA; 28762 MW; 3006017ED9B2F0E7 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
|||
Db 146 NWGPLV 151

RESULT 2
CAE78956 PRELIMINARY; PRT; 257 AA.
ID CAE78956; PRELIMINARY; PRT; 257 AA.
AC CAE78956;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE ABC-type transport system permease protein.
GN GLDF OR BD1024.
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,

RA Keller H., Lambert C., Evans K.J., Goemann A., Meyer F.,
 RA Sockett R.E., Schuster S.C.;
 RT "A predator unmasked: life cycle of *Bdellovibrio bacteriovorus* from a
 genomic perspective.";
 RL Science 303:689-692(2004).
 DR EMBL; BX842648; CAB78956.1; -.
 SQ SEQUENCE 257 AA; 28762 MW; 3006017ED9B2F0E7 CRC64;

Query Match 100.0%; Score 38; DB 2; Length 257;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
 |||||
 DB 146 NWGPLV 151

RESULT 3
 GLC4_SOYBN STANDARD; PRT; 562 AA.
 AC P02858
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Glycinin G4 precursor [Contains: Glycinin A5 subunit; Glycinin A4
 subunit; Glycinin B3 subunit].
 GN Name-GY4;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Bonninori;
 RA Hirano H., Fukazawa C., Harada K.;
 RT "The primary structures of the A4 and A5 subunits are highly
 homologous to that of the A3 subunit in the glycinin seed storage
 protein of soybean.";
 RT FEBS Lett. 181:124-128(1985).
 RN [3]
 RP SEQUENCE (A4/A5 SUBUNITS).
 RC STRAIN=cv. Bonninori;
 RA Hirano H., Fukazawa C., Harada K.;
 RT "The primary structures of the A4 and A5 subunits are highly
 homologous to that of the A3 subunit in the glycinin seed storage
 protein of soybean.";
 RT FEBS Lett. 181:124-128(1985).
 RN [3]
 RP SEQUENCE OF 181-386 FROM N.A.
 RC STRAIN=cv. CX635-1-1-1;
 RA Scallion B.J., Dickinson C.D., Nielsen N.C.;
 RT "Characterization of a null-allele for the G₄ glycinin gene from
 soybean.";
 RL Mol. Gen. Genet. 208:107-113(1987).
 CC -!- FUNCTION: Glycinin is the major seed storage protein of soybean.
 CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond.
 CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
 CC family.

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EMBL; X02626; CAA26478.1; -.
 EMBL; X05652; CAB57802.1; -.
 PIR; A91145; FWSYG5.

DR HSP; P04776; 1FXZ.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR011051; RmlC_like_cupin.
 DR InterPro; IPR006044; Seedstore_118.
 DR Pfam; PF00190; Cupin; 2.
 DR PRINTS; PR00439; 11SGLOBULIN.
 DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
 KW Direct protein sequencing; Multigene family; Seed storage protein;
 .Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 120
 FT CHAIN 121 377
 FT CHAIN 378 562
 FT CHAIN 562 562
 FT DISULFID 108 384
 FT CONFLICT 29 29
 FT CONFLICT 82 82
 FT CONFLICT 86 86
 FT CONFLICT 94 94
 FT CONFLICT 101 103
 FT CONFLICT 105 105
 FT CONFLICT 117 117
 FT CONFLICT 253 253
 FT CONFLICT 332 335
 FT CONFLICT 332 335
 SQ SEQUENCE 562 AA; 63587 MW; F5A06B8856B9BBD6 CRC64;

Query Match 100.0%; Score 38; DB 1; Length 562;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
 |||||
 DB 543 NWGPLV 548

RESULT 4
 Q43452 PRELIMINARY; PRT; 562 AA.
 AC Q43452;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Glycinin precursor.
 GN Name=Gy4;
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=92256811; PubMed=1316192;
 RA Xue Z.T., Xu M.L., Shen W., Zhuang N.L., Hu W.M., Shen S.C.;
 RT "Characterization of the G₄ Glycine gene from soybean Glycine max cv.
 Forrest.";
 RL Plant Mol. Biol. 18:897-908(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Hue Z.T.;
 RL Submitted (MAR-1990) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
 CC basic chain derived from a single precursor and linked by a
 CC disulfide bond (By similarity).
 CC -!- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
 CC family.
 CC EMBL; X52863; CAA37044.1; -.
 DR PIR; PQ0199; PQ0199.
 DR PIR; S20946; S20946.
 DR HSP; P04776; 1FXZ.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR006045; Cupin.
 DR InterPro; IPR011051; RmlC_like_cupin.

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DR InterPro; IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
KW Signal.
FT CHAIN 1 23 Potential.
FT CHAIN 24 562 glycinin.
SQ SEQUENCE 562 AA; 63876 MW; 3A4EF28E44B815A CRC64;
Query Match 100.0%; Score 38; DB 2; Length 562;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NWGPLV 6
DB 543 NWGPLV 548
|||||
PRT; 563 AA.
RESULT 5
Q39921 PRELIMINARY;
ID Q39921 PRELIMINARY; PRT; 563 AA.
AC Q39921;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ASA4B3 subunit.
OS Name-glycinin G4;
GN Glycine soja (Wild soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3848;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SH1;
RA Xue Z.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond (By similarity).
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
EMBL; X86970; CAA60533.1; -.
DR PIR; S54802; S54802.
DR HSP; P04776; 1FXZ.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR011051; RmlC like cupin.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
SQ SEQUENCE 563 AA; 63806 MW; EC171BED5F2B361F CRC64;
Query Match 100.0%; Score 38; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NWGPLV 6
DB 544 NWGPLV 549
|||||
PRT; 563 AA.
RESULT 6
Q9SB11 PRELIMINARY;
ID Q9SB11 PRELIMINARY; PRT; 563 AA.
AC Q9SB11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glycinin.
OS Glycine max (soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaves;
RA Chen S., Arahira M., Fukazawa C.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: Hexamer; each subunit is composed of an acidic and a
CC basic chain derived from a single precursor and linked by a
CC disulfide bond (By similarity).
CC -1- SIMILARITY: Belongs to the 11S seed storage protein (globulins)
CC family.
EMBL; AB004062; BAA74953.1; -.
DR PIR; PQ0199; PQ0199.
DR HSP; P04776; 1FXZ.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR006045; Cupin.
DR InterPro; IPR011051; RmlC like cupin.
DR InterPro; IPR006044; Seedstore_11s.
DR Pfam; PF00190; Cupin; 2.
DR PRINTS; PR00439; 11SGLOBULIN.
DR PROSITE; PS00305; 11S_SEED_STORAGE; 1.
SQ SEQUENCE 563 AA; 63797 MW; 4ACC765C55AB9E18 CRC64;
Query Match 100.0%; Score 38; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NWGPLV 6
DB 544 NWGPLV 549
|||||
PRT; 483 AA.
RESULT 7
Q6CLB6 PRELIMINARY;
ID Q6CLB6 PRELIMINARY; PRT; 483 AA.
AC Q6CLB6;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to ca|CA6037|CaERC4 Candida albicans ethionine resistance
DE protein.
DE ORFNames=KLLA0F04279g;
GN Kluyveromyces lactis (Yeast).
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boixame A., Boyer E., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozler-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Colicin A (Fragment).
GN Name=caa;
OS Escherichia coli.
OG Plasmid pColA9.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=87147231; PubMed=2434951;
RA Baty D., Knibiehler M., Verheij H., Pattus F., Shire D., Bernadac A.,
RA Lazdunski C.;
RT "Site-directed mutagenesis of the COOH-terminal region of colicin A:
RT effect on secretion and voltage-dependent channel activity";
RL Proc. Natl. Acad. Sci. U.S.A. 84:1152-1156(1987).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=92235820; PubMed=1373773;
RA Parker M.W., Postma J.P.M., Pattus F., Tucker A.D., Tsernoglou D.;
RT "Refined structure of the pore-forming domain of colicin A at 2.4-A
RT resolution.";
RL J. Mol. Biol. 224:639-657(1992).
RN [3]
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RP or send an email to license@isb-sib.ch).
RN [4]
RP EMBL; M15691; AAA23592.1; --
DR PIR; I53544; I41169.
DR PDB; 1COL; X-ray; A/B=1-204.
DR InterPro; IPR000293; Channel_colicin.
DR Pfam; PF01024; Colicin, 1.
DR PRINTS; PR00280; CHANNELCOLICIN
DR ProDom; PD002657; Channel_colicin; 1.
DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
KW 3D-structure; Antibiotic; Bacteriocin; Plasmid; Transmembrane.
FT NON TER 1
FT TRANSMEM 139 161 Potential.
FT TRANSMEM 165 187 Potential.
FT SEQUENCE 204 AA; 21790 MW; F7702455E2E4E9B9 CRC64;
SQ
Query Match 92.1%; Score 35; DB 1; Length 204;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NWGPLV 6
Db 129 NWGPLM 134
RESULT 12
ID Q7ZA77 PRELIMINARY; PRT; 378 AA.
AC Q7ZA77;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exo-arabinanase.
DN Name=abnx;
OS Penicillium chrysogenum (Penicillium notatum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium;

OC Penicillium chrysogenum complex.
OX NCBI_TaxID=5076;
RN [1]
RP SEQUENCE FROM N.A.
RA Inara H., Shibano A., Sakamoto T.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Hideshi I., Asako S., Tateuji S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB096108; BAC76689.1; --
DR InterPro; IPR002860; Glyco_hydro_BNR.
DR Pfam; PF02012; BNR; 2.
SQ SEQUENCE 378 AA; 41694 MW; C780B1E1F8BC8D2A CRC64;
Query Match 92.1%; Score 35; DB 2; Length 378;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NWGPLV 6
Db 211 NWGPPV 216
RESULT 13
ID CEAN_ECOLI STANDARD; PRT; 387 AA.
AC P08083;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Colicin N.
DE Namescna;
GN Escherichia coli.
OG Plasmid COLN pCHAP4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88201670; PubMed=2834623;
RA Pugsley A.P.;
RT "Nucleotide sequencing of the structural gene for colicin N reveals
RT homology between the catalytic, C-terminal domains of colicins A and
RT N.";
RL Mol. Microbiol. 1:317-325(1987).
RN [2]
RP SEQUENCE OF 372-387 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88174431; PubMed=3280946;
RA Pugsley A.P.;
RT "The immunity and lysis genes of ColN plasmid pCHAP4.";
RL Mol. Gen. Genet. 211:335-341(1988).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF 91-387.
RX MEDLINE=98362590; PubMed=9687368;
RA Vetter I.R., Parker M.W., Tucker A.D., Lakey J.H., Pattus F.,
RA Tsernoglou D.;
RT "Crystal structure of a colicin N fragment suggests a model for
RT toxicity.";
RL Structure 6:863-874(1998).
CC -1- FUNCTION: This colicin is a channel-forming colicin. This class of
CC transmembrane toxins depolarize the cytoplasmic membrane, leading
CC to dissipation of cellular energy.
CC -1- FUNCTION: Colicins are polypeptide toxins produced by and active
CC against, Escherichia coli and closely related bacteria.
CC -1- SIMILARITY: Belongs to the channel forming colicin family.
CC -----
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CC or send an email to license@isb-sib.ch).
RN [4]
RP EMBL; M15691; AAA23592.1; --
DR PIR; I53544; I41169.
DR PDB; 1COL; X-ray; A/B=1-204.
DR InterPro; IPR000293; Channel_colicin.
DR Pfam; PF01024; Colicin, 1.
DR PRINTS; PR00280; CHANNELCOLICIN
DR ProDom; PD002657; Channel_colicin; 1.
DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
KW 3D-structure; Antibiotic; Bacteriocin; Plasmid; Transmembrane.
FT NON TER 1
FT TRANSMEM 139 161 Potential.
FT TRANSMEM 165 187 Potential.
FT SEQUENCE 204 AA; 21790 MW; F7702455E2E4E9B9 CRC64;
SQ
Query Match 92.1%; Score 35; DB 1; Length 204;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NWGPLV 6
Db 129 NWGPLM 134
RESULT 12
ID Q7ZA77 PRELIMINARY; PRT; 378 AA.
AC Q7ZA77;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exo-arabinanase.
DN Name=abnx;
OS Penicillium chrysogenum (Penicillium notatum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium;

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DR EMBL; Y00533; CAA68592.1; -;
 DR EMBL; X06933; CAA30021.1; -;
 DR PIR; S00867; S00867;
 DR PDB; 1A87; X-ray; @=67-387;
 DR InterPro; IPR000293; Channel_colicin.
 DR Pfam; PF01024; Colicin; 1.
 DR PRINTS; PR00280; CHANLCOLICIN.
 DR ProDom; PD002657; Channel_colicin; 1.
 DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
 KW 3D-structure; Antibiotic; Bacteriocin; Plasmid; Transmembrane.
 FT DOMAIN 1 49
 FT TRANSMEM 325 345 Gly-rich.
 FT TRANSMEM 350 370 Potential.
 FT STRAND 93 94
 FT TURN 95 96
 FT TURN 97 101
 FT STRAND 103 104
 FT TURN 106 107
 FT STRAND 108 111
 FT HELIX 114 116
 FT TURN 117 119
 FT STRAND 122 128
 FT TURN 129 130
 FT STRAND 131 137
 FT TURN 140 141
 FT STRAND 143 148
 FT HELIX 149 151
 FT HELIX 153 155
 FT STRAND 157 161
 FT HELIX 170 214
 FT HELIX 216 230
 FT TURN 231 231
 FT HELIX 234 236
 FT HELIX 240 251
 FT TURN 252 252
 FT TURN 254 255
 FT HELIX 260 271
 FT TURN 272 272
 FT HELIX 275 283
 FT TURN 284 285
 FT HELIX 287 289
 FT TURN 292 293
 FT HELIX 294 309
 FT TURN 310 311
 FT HELIX 315 326
 FT TURN 327 328
 FT HELIX 331 343
 FT TURN 344 344
 FT TURN 348 349
 FT HELIX 352 370
 FT HELIX 372 385
 SQ SEQUENCE 387 AA; 1C4342E222F8CECD CRC64;

Query Match 92.1%; Score 35; DB 1; Length 387;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
 DB 313 NWGPLL 318

RESULT 14

Q9XB47 ID Q9XB47 PRELIMINARY; PRT; 499 AA.
 AC Q9XB47; (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Colicin S4.
 GN Names=csa;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9287842; PubMed=10348872;
 RA Pilsel H., Majs D., Braun V.;
 RT "Characterization of colicin S4 and its receptor OmpW, a minor protein
 of the Escherichia coli outer membrane.";
 RL J. Bacteriol. 181:3578-3581(1999).
 DR EMBL; Y18684; CAB46008.1; -;
 DR HSSP; P04480; 1COL.
 DR InterPro; IPR000293; Channel_colicin.
 DR InterPro; IPR001232; Skpl.
 DR Pfam; PF01024; Colicin; 1.
 DR PRINTS; PR00280; CHANLCOLICIN.
 DR ProDom; PD002657; Channel_colicin; 1.
 DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
 SQ SEQUENCE 499 AA; 54085 MW; 3E36C7271BF1D293 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 499;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NWGPLV 6
 DB 424 NWGPLM 429

RESULT 15

CEAB_ECOLI ID CEAB_ECOLI STANDARD; PRT; 510 AA.
 AC P05819;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Colicin B.
 GN Name=cba;
 OS Escherichia coli.
 OG Plasmid ColBM-pF166.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87250309; PubMed=2439491;
 RA Schramm E., Mende J., Braun V., Kamp R.M.;
 RT "Nucleotide sequence of the colicin B activity gene cba: consensus
 pentapeptide among TonB-dependent colicins and receptors.";
 RL J. Bacteriol. 169:3350-3357(1987).
 CC -!- FUNCTION: This colicin is a channel-forming colicin. This class of
 transmembrane toxins depolarize the cytoplasmic membrane, leading
 to dissipation of cellular energy.
 CC -!- FUNCTION: Colicins are polypeptide toxins produced by and active
 against Escherichia coli and closely related bacteria.
 CC -!- MISCELLANEOUS: This colicin requires tonB for its uptake.
 CC -!- SIMILARITY: Belongs to the channel forming colicin family.
 CC -----
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DR EMBL; M16816; AAA98063.1; -;
 DR PIR; A27089; IKECBB.
 DR HSSP; P04480; 1COL.
 DR InterPro; IPR000293; Channel_colicin.

DR InterPro; IPR003058; Cloacin.
DR InterPro; IPR010916; TonB_Box_N.
DR InterPro; IPR010917; TonB_recept_C.
DR Pfam; PF03515; Cloacin; 1.
DR Pfam; PF01024; Colicin; 1.
DR PRINTS; PR00280; CHANCOLICIN.
DR PRINTS; PR01295; CLOACIN.
DR ProDom; PD002657; Channel_colicin; 1.
DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
DR PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
DR PROSITE; PS01156; TONB_DEPENDENT_REC_2; FALSE_NEG.
KW Antibiotic; Bacteriocin; Direct protein sequencing; Plasmid; TonB box;
KW Transmembrane.
FT INIT_MET 0 0
FT SITE_16 23 TonB box.
FT TRANSMEM 454 474 Potential.
FT TRANSMEM 476 496 Potential.
SQ SEQUENCE 510 AA; 54732 MW; 6E4B972CF19245F1 CRC64;

Query Match 92.1%; Score 35; DB 1; Length 510;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NWGPLV 6
Db 438 NWGPLM 443

Search completed: November 6, 2004, 19:52:51
Job time : 83.25 secs

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